	SEQUENCE LISTING
0/	(1) GENERAL INFORMATION:
	(i) APPLICANT: Meissner, Paul S. Coleman, Timothy A.
5/	(ii) TITLE OF INVENTION: HUMAN CRIPTIN GROWTH FACTOR
	(iii) NUMBER OF SEQUENCES: 7
	(iv) CORRESPONDENCE ADDRESS: (A) ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, STEWART & OLSTEIN (B) STREET: 6 Becker Farm Road (C) CITY: Roseland (D) STATE: N.J. (E) COUNTRY: U.S.A (F) ZIP: 07068
4.02.1111	(v) COMPUTER READABLE FORM: (A) MEDIUM TYPE: Floppy disk (B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
	(vi) CURRENT APPLICATION DATA: (A) APPLICATION NUMBER: US 08/471,371 (B) FILING DATE: 06-JUN-1995 (C) CLASSIFICATION:
4, 4,	(viii) ATTORNEY/AGENT INFORMATION: (A) NAME: Ferraro, Gregory D. (B) REGISTRATION NUMBER: 36,134 (C) REFERENCE/DOCKET NUMBER: 32580-455
	(ix) TELECOMMUNICATION THEORMATION: (A) TELEPHONE: 1994-1700 (B) TELEFAX: (201) 1994-1744
jo Lj	(2) INFORMATION FOR SEQ ID NO:1:\
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 774 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: cDNA
	(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:\
ATGCAGAAGA CTCTTCAAGA TTCAGCTTTC CTGGAAACTG ATCTTCAATG CACTAAGAGA

(A) NAME/KEY: CDS
(B) LOCATION: 82..771

AGGAGACTCT CAAACCCAAA A ATG ACC TGG AGG CAC CAT GTC AGG CTT CTG
Met Thr Trp Arg His His Val Arg Leu
1 10

60 111

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TTT Phe	ACG Thr	GTC Val	AGT Ser	TTG Leu 15	GCA Ala	TTA (Leu (CAG Gln	ATC Ile	ATC Ile 20	AAT Asn	TTG Leu	GGA	AAC Asn	Ser 25	Tyr	133
caa Gln	AGA Arg	GAG Glu	AAA Lys 30	CAT His	AAC Asn	GGC Gly	GGT Gly	AGA Arg 35	GAG Glu	GAA Glu	GTC Val	ACC Thr	AAG Lys 40	GTT Val	GCC Ala	207
ACT Thr	CAG Gln	AAG Lys \ 45	His	CGA Arg	CAG	TCA Ser	CCG Pro 50	CTC Leu	AAC Asn	TGG Trp	ACC Thr	TCC Ser 55	AGT Ser	CAT	TTC Phe	255
GGA Gly	GAG Glu 60	Val	ACT Thr	GGG	AGC Ser	GCC Ala 65	GAG Glu	GGC Gly	TGG Trp	GGG Gly	CCG Pro .70		GAG Glu	ĊCG Pro	CTC Leu	303
CCC Pro	Tyr	TCC Ser	CGG Arg	GCT Ala	TTC Phe 80	GGA Gly	GAG Glu	GGT Gly	GCG Ala	TCC Ser 85		CGG Arg	CCG Pro	CGC	TGC Cys 90	351
TGC Cys	AGG Arg	AAC Asr	GGC GGC	GGT Gly 95	runr	TGC Cys	GTG Val	CTG Leu	GGC Gly 100	001	TTC Phe	TGC Cys	GTG Val	TGC Cys 105	CCG Pro	399
GCC	CAC His	TTO Phe	C ACC e Thi	c GT?	Y Wid	TAC Tyr	TGC Cys	GAG Glu 115	11112	GAC Asp	CAC Glr	AGG Arg	G CGC G Arg 120	AGT Sei	r GAA c Glu	447
TG(Cys	GGG Gl	C GCG Y Ala	a Le	G GA(u Gl	G CAC	GGA	GCC Ala		ACC Thi	CTC Lev	CGC Arg	GCC G Ala 13!	TGC a Cys 5	CAC S His	C CTC s Leu	495
TG(Cy:	C AG S Ar	g Cy	C AT s Il	C TTO	c GGG	GCC Ala	ner	CAC His	TG(S Cys	C CTO	C CC 1 Pr 15	C CTO O Le	C CAG	G AC	G CCT r Pro	543
GA As:	C CG p Ar		T GA s As	c cc p Pr	G AAA o Lys	S WOF	TT(c Le	G GCC u Ala	TCC a Se:		C GC s Al	т СА а Ні	C GG s Gl	G CCC y Pro 170	591 5
		C GG a Gl	G GG y Gl	SC GC y Al	a Pr	C AGO Sei	CTC	G CT u Le	A CT u L'e 18	u nc	G CT u Le	G CC	C TG	C GC s Al	A ACT a Thi	r 639 r
CC Pr	T GC	A CO a Pr	co A.	CC TC la Se	C TG	C GCC s Ala	C CG a Ar	G AT g Me		g Pr	G CG	C AC	CC CT nr Le 20	C GC u G]	T CCC Ly Pr	C 687
TC Tr	G TO	er Le	rr Co eu P: 05	CG TC ro Se	CC TC er Se	C AG r Se	C GG r Gl 21	y 56	GC GG er Gl	C GC y Al	c co la Pa	CT GC ro Al	CG G# la G] 15	AA GO Lu G	GC CG ly Ar	G 735 g
G/ As	sp L	rg G eu G 20	GC A' ly I	TC GO	CC TT la Ph	T AA e As 22	11 F1.	T CT ie Le	TA TO ∋u Cy	TC Ys C		AA T ys 30	A.A.			774
													/			

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 230 amino acids

 (B) TYPE: amino acid

 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Thr Trp Arg His His Val Arg Leu Leu Phe Thr Val Ser Leu Ala

Leu Gln Tle Ile Asn Leu Gly Asn Ser Tyr Gln Arg Glu Lys His Asn 25 30

Gly Gly Arg Glu Glu Val Thr Lys Val Ala Thr Gln Lys His Arg Gln 35 40

Ser Pro Leu Asn Trp Thr Ser Ser His Phe Gly Glu Val Thr Gly Ser 50 60

Ala Glu Gly Trp Gly Pro Glu Glu Pro Leu Pro Tyr Ser Arg Ala Phe
65 70 75 80

Gly Glu Gly Ala Ser Ala Arg Pro Arg Cys Cys Arg Asn Gly Gly Thr

Cys Val Leu Gly Ser Phe Cys Val Cys Pro Ala His Phe Thr Gly Arg

Tyr Cys Glu His Asp Gln Arg Arg Ser Glu Cys Gly Ala Leu Glu His 115 120 125

Gly Ala Trp Thr Leu Arg Ala Cys His Leu Cys Arg Cys Ile Phe Gly

Ala Leu His Cys Leu Pro Leu Gln Thr Pro Asp Arg Cys Asp Pro Lys 145 150 155 160

Asp Phe Leu Ala Ser His Ala His Gly Pro Ser Ala Gly Gly Ala Pro 175

Ser Leu Leu Leu Leu Leu Pro Cys Ala Thr Pro Ala Pro Ala Ser Cys

Ala Arg Met Arg Pro Arg Thr Leu Gly Pro Trp Ser Leu Pro Ser Ser 195 200 205

Ser Gly Ser Gly Ala Pro Ala Glu Gly Arg Asp Leu Gly Ile Ala Phe

Asn Phe Leu Cys Cys Lys 225 230

- (2) INFORMATION FOR SEQ ID NO:3:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "PRIMER"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ACTCTTGGAT CCAATTTGGG AAACAGCTATC AAAGA

- (2) INFORMATION FOR SEQ ID NO:4:
 - (i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 42 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: other nucleic acid</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
TACAACTCTA GACTATTATT TACAACATAG AAAATTAAAG GC	42
(2) INFORMATION FOR SEQ ID NO:5:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "PRIMER"	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
ACTCTTGGAT CCGCCATCAT GACCTGGAGG CACCAT	36
(2) INFORMATION FOR SEQ TO NO:6:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS:\single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: other\nucleic acid (A) DESCRIPTION: /desc = "PRIMER"	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
TACAACCAGC TGCTATTATT TACAACATAG	30
(2) INFORMATION FOR SEQ ID NO:7:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 188 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: protein	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	
Met Asp Cys Arg Lys Met Ala Arg Phe Ser Tyr Ser Val Ile Trp Ile	

 Met
 Ala
 Ile
 Ser
 Lys
 Val
 Phe
 Glu
 Leu
 Gly
 Leu
 Val
 Ala
 Gly
 Jeu
 Ala
 Phe
 Arg
 Arg
 Arg
 Fur
 Leu
 Ala
 Phe
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 Arg
 Arg
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